

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:03 ; Search time 35 Seconds
(without alignments)
2307.728 Million cell updates/sec

Title: US-09-935-124a-2

Perfect score: 2018
Sequence: 1 MDLFGDLPPEPSPRPAAGK.....KAVQSGADNVTMVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_Archea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Xvirus:*
16: SP_Bacteriophage:*
17: SP_Archea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	382	4 Q9H0C8	Q9H0C8 homo sapien
2	1935	95.9	382	11 Q8R0R6	Q8R0R6 mus musculi
3	1931	95.7	382	11 Q8R0R6	Q8R0R6 mus musculi
4	1886	68.7	272	11 Q8D0C9	Q8D0C9 mus musculi
5	1078	53.4	212	11 Q8C5A6	Q8C5A6 mus musculi
6	856	42.4	167	11 Q8Z0T2	Q8Z0T2 mus musculi
7	481	23.8	341	10 Q9LMT1	Q9LMT1 arabidopsis
8	480	23.8	351	10 Q944K0	Q944K0 arabidopsis
9	474	23.5	242	5 Q62212	Q62212 caenorhabdi
10	408.5	20.2	319	10 Q8S8Z0	Q8S8Z0 mesembryant
11	398.5	19.7	311	10 Q8R3V3	Q8R3V3 arabidopsis
12	381.5	18.9	243	10 Q8S3P1	Q8S3P1 oryza sativ
13	368.5	18.3	420	10 Q8VZD9	Q8VZD9 arabidopsis
14	368	18.2	389	10 Q81773	Q81773 arabidopsis
15	368	18.2	975	5 O15743	O15743 dictyostell
16	366.5	18.2	420	10 Q94AT1	Q94AT1 arabidopsis

17	366.5	18.2	757	4 Q9UPT0	Q9UPT0 homo sapien
18	365	18.1	359	10 Q82469	Q82469 mesembryant
19	365	18.1	766	4 Q8WY54	Q8WY54 homo sapien
20	364.5	18.1	348	10 Q91EW5	Q91EW5 arabidopsis
21	364.5	18.1	371	10 Q8VZD9	Q8VZD9 arabidopsis
22	362	17.9	464	10 Q8VZD9	Q8VZD9 arabidopsis
23	361	17.9	380	10 Q8R3V3	Q8R3V3 arabidopsis
24	359.5	17.8	454	4 Q86PM2	Q86PM2 homo sapien
25	358.5	17.8	361	10 Q9SD02	Q9SD02 arabidopsis
26	353.5	17.5	355	10 Q81716	Q81716 arabidopsis
27	353.5	17.5	362	10 Q8ZP19	Q8ZP19 lotus japon
28	352	17.4	302	10 Q8GCM4	Q8GCM4 arabidopsis
29	352	17.4	322	10 Q9SLA1	Q9SLA1 arabidopsis
30	351	17.4	404	10 Q82200	Q82200 arabidopsis
31	351	17.4	658	10 Q940A2	Q940A2 arabidopsis
32	350	17.3	305	10 Q942N4	Q942N4 oryza sativ
33	350	17.3	357	10 Q8S2S3	Q8S2S3 arabidopsis
34	341.5	16.9	450	11 Q9WVR7	Q9WVR7 ratius norv
35	339	16.8	396	10 Q9LPI2	Q9LPI2 arabidopsis
36	338.5	16.8	383	10 Q9M1P8	Q9M1P8 arabidopsis
37	338.5	16.8	390	10 Q9XEB8	Q9XEB8 arabidopsis
38	338.5	16.8	405	10 Q91MK9	Q91MK9 arabidopsis
39	338	16.7	323	11 Q9E0E2	Q9E0E2 mus musculi
40	338	16.7	326	11 Q9E0E3	Q9E0E3 mus musculi
41	338	16.7	326	11 Q8R4T7	Q8R4T7 mus musculi
42	337.5	16.7	380	10 Q82468	Q82468 mesembryant
43	337.5	16.7	380	10 P93006	P93006 arabidopsis
44	336.5	16.7	381	10 Q24078	Q24078 medicago sa
45	336.5	16.7	396	10 Q80871	Q80871 arabidopsis

ALIGNMENTS

RESULT 1
Q9H0C8 PRELIMINARY; PRT; 392 AA.
ID Q9H0C8
AC Q9H0C8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 42.9 kDa protein (Integrin-linked kinase-associated serine/threonine phosphatase 2C).
GN DKFZP434J2031.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP LEUNG-HAGSTEDT, C., Mahendra A., Naruszewicz I., Hannigan G.E.;
RA "Mediation of Integrin signal transduction by ILKAP, a protein
RT phosphatase 2C associating with the Integrin-linked kinase, ILK1".
RL EMBL J. 0:0-0(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN EMBL; AL136850; CAB6784.1; -;
DR EMBL; AY024365; AAK07736.1; -;
DR EMBL; BC006576; AAH06576.1; -;
DR HSSP; P35813; IAO6.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR SMART; SM00331; PP2C_Sig; 1.

DR PROSITE; PS01032; PP2C; 1.
 KM Hypothetical protein; Kinase.
 SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
 Best Local Similarity 100.0%; Pred. No. 4,4e-156;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 DB 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180
 DB 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 DB 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 DB 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392

RESULT 2

QY 08R0F6 PRELIMINARY; PRT; 392 AA.
 AC 08R0F6;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Similar to protein phosphatase 2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

(1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strauberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026953; AAH26953.1; -
 SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC9B7176 CRC64;

Query Match 95.8%; Score 1935; DB 11; Length 392;
 Best Local Similarity 95.2%; Pred. No. 2,5e-149;
 Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 DB 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180
 DB 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 DB 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 DB 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392

RESULT 3

QY 09Z1Z6 PRELIMINARY; PRT; 392 AA.
 AC 09Z1Z6;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Protein phosphatase 2C.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99074314; PubMed=9857069;
 RA Tong Y., Quilston R., Shen S.H.;
 RT "Cloning and characterization of a novel mammalian PP2C isozyme."
 RL J. Biol. Chem. 273:35282-35290(1998).
 DR EMBL; AF095927; AAC97497.1; -
 DR HSSP; P35813; 1A60.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C; SIG. 1.
 DR PROSITE; PS01032; PP2C; 1.
 SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
 Best Local Similarity 95.2%; Pred. No. 5,3e-149;
 Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 DB 61 SLATSSIQWVKTGEGKAKRTTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180
 DB 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGIGIRASKFAAQNHLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 DB 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 DB 241 LCRVNEESQKHAALSLSKENHPQYEEERMRIOKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLDEKIQTRREGKSAAD 360

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QY 361 ARYEACNRLANKAVQSGADNVTWVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTWVRIGH 392

RESULT 4
Q9DC99 PRELIMINARY; PRT; 272 AA.
AC Q9DC99;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 0710007A14R1K protein.
GN 0710007A14R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK003007; BAB22508.1; -.
DR HSSP: P35813; IAEQ; 0710007A14R1K.
DR MGI: MGI:1914694; 0710007A14R1K.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 272 AA; 30279 MW; 485F2959D91BA63D CRC64;

Query Match 68.7%; Score 1386; DB 11; Length 272;
Best Local Similarity 97.8%; Pred. No. 7.3e-105;
Matches 266; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 121 MODAHVILNDITEECRPPSSLTTRVSYFAVFDGIGGIRASKFAQNLHONLRKFPKGDV 180
DB 1 MODAHVILNDITEECRPPSSLTTRVSYFAVFDGIGGIRASKFAQNLHONLRKFPKGDV 60
QY 181 ISVEKTVKRCCLDPTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 240
DB 61 ISVEKTVKRCCLDPTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 120
QY 241 LCRYNEESQKAAALSKENHPTQYEEERRIIOKAGNVDRGVGLVEVRSISIGDQYKR 300
DB 121 LCRYNEESQKAAALSKENHPTQYEEERRIIOKAGNVDRGVGLVEVRSISIGDQYKR 180
QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 360
DB 181 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 240
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QY 361 ARYEACNRLANKAVQSGADNVTWVRIGH 392
DB 241 ARYEACNRLANKAVQSGADNVTWVRIGH 272

RESULT 5
Q9CS46 PRELIMINARY; PRT; 212 AA.
AC Q9CS46;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 0710007A14R1K protein (Fragment).
GN 0710007A14R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMERYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK019158; BAB31574.1; -.
DR HSSP: P35813; IAEQ; 0710007A14R1K.
DR MGI: MGI:1914694; 0710007A14R1K.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR NON_TER 1.
FT
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Query Match 53.4%; Score 1078; DB 11; Length 212;
Best Local Similarity 98.1%; Pred. No. 6.1e-80;
Matches 208; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 181 ISVEKTVKRCCLDPTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 240
DB 1 ISVEKTVKRCCLDPTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 60
QY 241 LCRYNEESQKAAALSKENHPTQYEEERRIIOKAGNVDRGVGLVEVRSISIGDQYKR 300
DB 61 LCRYNEESQKAAALSKENHPTQYEEERRIIOKAGNVDRGVGLVEVRSISIGDQYKR 120
QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 360
DB 121 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 180
QY 361 ARYEACNRLANKAVQSGADNVTWVRIGH 392
DB 181 ARYEACNRLANKAVQSGADNVTWVRIGH 212

RESULT 6
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Q920T2 ID Q920T2 PRELIMINARY; PRT; 167 AA.
 AC Q920T2;
 DT 01-MAY-1999 (TREMBlrel. 10, Last Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 18.8 kDa protein (Fragment).
 GN 0710007A1AR1K.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=LUNG;
 RA Stothard P.M., Pilgrim D.;
 RT "Isolation of PP2C sequences using degenerate-oligo PCR."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF117831; AAD17234.1; -.
 DP HSSP; P35813; 1A6Q.
 MGDI: MG1:1914694; 0710007A1AR1K.
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2EFB09DD95B CRC64;
 Query Match 42.4%; Score 856; DB 11; Length 167;
 Best Local Similarity 98.8%; Pred. No. 5,1e-62;
 Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 157 IRASKFAQVQLHQLVIRKPKGVISVEKTVKRCLELTFPHHTBEFLPKASSOKPAWKDG 216
 DB 1 IRASKFAQVQLHQLVIRKPKGVISVEKTVKRCLELTFPHHTBEFLPKASSOKPAWKDG 60
 QY 217 STATCVLAVNLIYIANLIGDSRAILCRYNESQKHAALSLSKENHPQYEEEMRIQKAGG 276
 DB 61 STATCVLAVNLIYIANLIGDSRAILCRYNESQKHAALSLSKENHPQYEEEMRIQKAGG 120
 QY 277 NVBDRGLVLEVSRSIGDQYKRCGTVSPDIRRCOLTPNDRFILL 323
 DB 121 NVBDRGLVLEVSRSIGDQYKRCGTVSPDIRRCOLTPNDRFILL 167
 RESULT 7
 Q9LMT1 PRELIMINARY; PRT; 341 AA.
 AC Q9LMT1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE T10F20.4 protein.
 GN T10F20.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=CV, COLUMBIA.
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vayberg M.,
 RA Altali H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federici N.A., Theologis A.;
 RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC034107; AAF97840.1; -.
 DR HSSP; P35813; 1A6Q.

DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C; 1.
 SQ SEQUENCE 341 AA; 37367 MW; 6873C0CE82310195 CRC64;
 Query Match 23.8%; Score 481; DB 10; Length 341;
 Best Local Similarity 35.8%; Pred. No. 4.9e-31;
 Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
 QY 78 KRTTSEENKNGSELY-----EKVCKASSV-----FLKGVYARKKGEREMQAHYI 127
 DB 24 KAKKSEEVGGGGAVAAGNREAEEDKPSFVSEKKEFLVEADVAEDKGAHRTMEDVWVV 83
 QY 128 LNDITECRPPSSLIRVGFVAFVFDGHGIRASKFAQVQLHQLVIRKPKGVISVEKTV 187
 DB 84 LPASLDF--PGLT--RCHAFALYDGHGRLAEPFKKHLHLNVLSAGLPRELLDV-KVA 138
 QY 188 KRCLDTFPHHTBEFLPKASSOKPAWKDGSTATCVLAVNLIYIANLIGDSRAILCR---- 243
 DB 139 KKAILEGFRITDELLOKSVS--GWDGATVACVWILDQKVFVANIGDAKAVLABSSST 196
 QY 244 -----YNESQKHAALSLSKENHPQYEEEMRIQKAGGV-RDGRVLGVLEVSRSIGDQ 297
 DB 197 NELGNHTTEAGNPVKAIVLTREHVAIYPOERSRIQKSGVSSNGRLQVLEVSRAFGDRH 256
 QY 298 YKRCGTVSPDIRRCOLTPNDRFILLACDGLPKVFTPEEAVNFIISLCLEDEKIOTREKGS 357
 DB 257 FKFGVSATPDHAFELTERENFMILGCDGLMEVFSPSDAVGVQTL-----KEG-- 307
 QY 358 AADARYEAACNRIANKAV-QRGSADNVTVWV 388
 DB 308 ---LHVSTVSRRLVKEAVKERRCKDCTAIVI 336
 RESULT 8
 Q944KO PRELIMINARY; PRT; 351 AA.
 AC Q944KO;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE A1G18030/T10F20.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natsumaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF428352; AAL16282.1; -.
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C; 1.
 SQ SEQUENCE 351 AA; 38514 MW; AFE224E0E003229 CRC64;
 Query Match 23.8%; Score 480; DB 10; Length 351;
 Best Local Similarity 35.8%; Pred. No. 6,1e-31;
 Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
 QY 78 KRTTSEENKNGSELY-----EKVCKASSV-----FLKGVYARKKGEREMQAHYI 127
 DB 34 KAKKSEEVGGGGAVAAGNREAEEDKPSFVSEKKEFLVEADVAEDKGAHRTMEDVWVV 93

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QY 82 SEEKNSSELV-----EKVCASAVIFGLKGVAAERKREEMODAVILN--DIIEEC 135
Db 3 SDSKRSKSDLLINDNSDESKKPRESNILYCTLAAYGCRKGERADMODTHMLPKFDLGE- 61
QY 136 RPPSSLLTRYSYAVVDGGGIGIRASKFAQNLOHNLIRKPK--GVISVEKTVRCILDT 194
Db 62 ---KSPISRSFPAITIDGHAGPRAAHGOSOMKQVYKELAFSDFPILTSLKQPTES 118
QY 195 FKHIDDEFILQASOSQKPAKMGSTPTCVLAVNDVILITALGSRALICRYNESQKHAL 254
Db 119 IYAVDDGFLAIAQNFYIMKQDSTIRATHTILNNVITVANIIGSRVARKKEDG-STAPY 177
QY 255 SLSEKHNPTOYEBERRIQAGAGVBDGVLGLEVSRSIGDQYKRCGVTSVPDIRRCQ 314
Db 178 CLTYADHPMSHDERMIQKAGAVVKDRINGVIEVRSISGDLPEKSLGISTPLKRLTL 237
QY 315 TPND 318
Db 238 TKND 241
RESULT 10
08S820
AC 08S820 PRELIMINARY; PRT; 319 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Protein phosphatase 2C.
GN MPC3
OS Mesembryanthemum crystallinum (Common ice plant).
OC Burkholderia, Vibrionellaceae, Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum;
OX NCBI_Taxid35344;
RN 11
RP SEQUENCE FROM N.A.
RA Miyazaki S., Izumi S., Fukuhara T., Bohmert H.J.;
RT "Plant Protein Phosphatases 2C ? A large protein family serving
RT complex functions."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083482; BAB88944.1; -.
SQ SEQUENCE 319 AA; 34477 MW; 0BD228603E34CFB0 CRC64;
Query Match 20.2%; Score 408.5; DB 10; Length 319;
Best Local Similarity 39.6%; Pred. No. 3.5e-25;
Matches 113; Conservative 41; Mismatches 86; Indels 45; Gaps 12
QY 109 GYVAERGEREERQDAHVILNDITEGCRPSSILITRVSYFAVFDGCGIRASKFAQNLT 168
Db 35 GY-ASSPKKSSMEDYEYETRIDGVAG-----EYVGLFGVFDGCGARRAAEYVKNLRF 85
QY 169 ONLIRKPKKDVIVSEKTVKRCILDTPKHTDEEFLQASOSQKPAKMD-GSTATCVLAVDN 227
Db 86 SNLI-KHPK--FIS---DTKSAIAEAYHTHDSFLKSENTQN---RDAGSTATLIVGD 136
QY 228 ILITANIGDSRALICRYNESQKHAALSLSEHNPTOYEBERRIQAGANVR---DORVL 284
Db 137 RLIVANQDSDRAIYICGSE-----AIVSRDKHPQDSERQRIEDAGGFMAAGTIRVG 190
QY 285 GYLVKSSIGDQYKRCGVTSVPDIRRCQLTPNDRFILACGLCFKVTTPBEANFLSC 344
Db 191 GYLVASAPFDKLLKQY-VVADPEIQEEVVDSSLEFILLASGLMDVVTNEEAVTNV--- 246
QY 345 LEDEKIOTREGKSADARYEAACNLANKAVQSGADNVTVMVR 389
Db 247 -----KPIQDT--EEAKKLMQEAQYQSGADNITCVVR 278
RESULT 11
08RXY3
ID 08RXY3 PRELIMINARY; PRT; 311 AA.
OC 08RXY3;

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DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 33.2 kDa protein.
 GN ATAG31750.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ichida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam C., Lin J.,
 RA Miranda M., Narasaka M., Nguyen N., Palm C.J., Sakurai T., Saito M.,
 RA Seki M., Shimizu F., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 DB "Arabidopsis Full length cDNA clones."
 DB Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DB EMBL: AY080658; AAL86334.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 311 AA; 33247 MW; 5E3098E91F116BFD CRC64;
 Query Match 19.7%; Score 398.5; DB 10; Length 311;
 Best Local Similarity 39.3%; Pred. No. 2.2e-24;
 Matches 112; Conservative 40; Mismatches 88; Indels 45; Gaps 12;
 QY 109 GYAERKGEERENDAHVILNDITECRPPSSILTRSYAFVFGHGIRASKAAONLH 168
 ID Q8VZD9; PRELIMINARY; PRT; 243 AA.
 AC Q8VZD9;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 26.7 kDa protein.
 GN 24K23.16
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzaceae; Oryza.
 NCBI_TaxId=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV, NIPONBARE;
 RA Park Y.-D., Roscoe N., Ramakrishna W., Sammiquel P., Shiloff B.,
 RA Ma J., Jiang Z., Kleinhofs A., Bennett J.;
 RT "Sequence characterization of orthologous regions in the barley and
 rice genomes."
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF480497; AAL87187.1; -

KW Hypothetical protein.
 SQ SEQUENCE 243 AA; 26734 MW; 8B481E17F559CSEF CRC64;
 Query Match 18.9%; Score 381.5; DB 10; Length 243;
 Best Local Similarity 37.9%; Pred. No. 3.8e-23;
 Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;
 QY 145 VSYFAVFDGHCGRASKFAAONLHILIR--KPPKGVISVEKTVKCLDTFKHTDEEF 202
 ID IGLFVFDGHCGRASKFAAONLHILIR--KPPKGVISVEKTVKCLDTFKHTDEEF 202
 DB 17 IGLFVFDGHCGRASKFAAONLHILIR--KPPKGVISVEKTVKCLDTFKHTDEEF 68
 QY 203 LKQASQKPAWKDGTATCYLAVNDILYANLDSRAILCRVNEESOKHAALSKEHNP 262
 DB 69 LKQASQKPAWKDGTATCYLAVNDILYANLDSRAILCRVNEESOKHAALSKEHNP 119
 QY 263 TOYEEMRIQKAGANVR---DGRVLGVLEYSRISGQVRCGVTSVPDIRCOLTPNDR 319
 DB 120 DQTEKRIEDAGCFVMAWGTWVGGLAVSRFGDLKQYVVD--PEIREVIDHSLE 178
 QY 320 FILACDGLFKVTPPEAVNFILSCLEDEKIQREGKSAADARYEACNLRANKAVORGS 379
 DB 179 FILACDGLFKVTPPEAVNFILSCLEDEKIQREGKSAADARYEACNLRANKAVORGS 222
 QY 380 ADVNTVAVRIGH 392
 DB 223 SDNITCVVRFELH 235
 RESULT 13
 Q8VZD9; PRELIMINARY; PRT; 420 AA.
 AC Q8VZD9;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ichida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narasaka M., Saito M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Saito M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY065026; AAL57666.1; -
 DR InterPro: IPR000222; PP2C-
 DR Pfam: PF00481; PP2C-1.
 DR SMART: SM00332; PP2C-1.
 DR SMART: SM00331; PP2C-SIG. 1.
 DR PROSITE: PS01032; PP2C; UNKNOWN 1.
 SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;
 Query Match 18.3%; Score 368.5; DB 10; Length 420;
 Best Local Similarity 32.8%; Pred. No. 9.5e-22;
 Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;
 QY 64 TSISQVKTGKGAKKTESEKNGSEELVEKKVCASSVIFGLK-----GYAERK 115
 DB 58 TSISQVKTGKGAKKTESEKNGSEELVEKKVCASSVIFGLK-----GYAERK 108
 QY 116 GEREEMQDAHVILNDITECRPPSSILTRSYAFVFGHGIRASKFAAONLHILIRK 175
 DB 109 GKRSTMEFDIKASTIEG-----QAVCMGIFDGHGSGRAAEYLKXELHPLNLM-KH 159

QY 176 PKGVISVEKTVKRCCLDTFKTDEEFLKQASSQKPAWK-DGSTATCVLAUNILYIANL 234
 DB 160 PQ-----FLDTTKALAEIRYKQDVAFLE---SEKDYTRDGGSTASAAVLVGNHLVYVNV 211
 QY 235 GDSRAILCRINESQKHAALSKEHNPTQYEEBMRIOKAGGNVR--DGRVLGVLEVR 291
 DB 212 GDSRTIV-----SKGAKAIALSDHKPRSDERRKIESAGVIMAGTWKRGVLAWSR 265
 QY 232 SIGDQYKRCGVTSVPDIRRCQLTTPNDRFILLACDGLPKVFTPEEAVNFILSCLEDEKIQ 351
 DB 266 ALGNRMKQF-VVAEPIQDLEIDHEALVLAISDGLMDVVPNEADV--ALAQSEEP-- 320
 QY 352 TREGSADARYEACNRLANKAVORGSAADNTVAVVRIGH 392
 DB 321 -----EAAARKLDTAFSGSADNITCIVVKFRH 349

RESULT 14

081773 PRELIMINARY; PRT; 389 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 42.6 kDa protein.
 GN F28M20.60 OR ATAG31750
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae;
 OC Ericales; Il; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_TaxId=3702;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hohnselt J.,
 RA Wewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Wewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN 131
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031004; CAA19748.1; -
 DR HSSP; P35813; IAG0.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C_1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 DR PROSITE; PS01032; PP2C_1.
 KW Hypothetical protein.
 SQ SEQUENCE 389 AA; 42562 MW; A7C4C39764BECIDEA CRC64;

Query Match 18.2%; Score 368; DB 10; Length 389;
 Best Local Similarity 33.7%; Pred. No. 9.3e-22;
 Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;
 QY 109 GYVAERGEREEMQDAHVILNDITEECRPSSLLITRVSYAVFDHGGRASKFAAONLH 168
 DB 60 GY-ASSPKRRSMEDYERIRIGVGG-----EIVGLFGVFDHGGRARAAYVKQLF 110
 QY 169 QNLIRKPKGDVISEKTVKRCCLDTFKTDEEFLKQASSQKPAWKD-GSTATCVLAVDN 227
 DB 111 SNLIR-HRK--FIS---DTTAAIADAVYQGTSEFLKSENSQN---RDASTASTAILVGD 161
 QY 228 ILVLIANLGSRAILCRYNESQKHAALSKEHNPTQYEEBMRIOKAGGNVR--DGRVL 284

DB 162 RLIVANVGSRVLCRGN-----AIAVSRKHDPQSDERKQIEDAGGVWAGTWKRGV 215
 QY 285 GVLEVSRSITGQYKRCGVTSVPDIR----- 310
 DB 216 GVLAASRAFGPRLKQF-VVADEPIQVLTFCOMLLYIKNATLLTTEHNLWISIVSL 274
 QY 311 -----RCQLTTPNDR-----FILLACDGLPKVFTPEEAVNFILSCLEDEKIQ 351
 DB 275 NGTLONFLRSLSISNGFQOEKVDSSLLEFLILIASDGLMDVVSNEEAVGMI-KAIEDP-- 330
 QY 352 TREGSADARYEACNRLANKAVORGSAADNTVAVVR 389
 DB 331 -----EEGARKLMMEAYVORGSAADNITCVVR 356

RESULT 15

015743 PRELIMINARY; PRT; 975 AA.

AC 015743
 DT 01-JUN-1998 (TREMBLrel. 05, Created)
 DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Spalten.
 GN SPVA
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OK NCBI_TaxId=44689;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=98252837; PubMed=9585512;
 RA Aubry L., Firtel R.A.;
 RT "Spalten, a protein containing Galpha-protein-like and pp2c domains,
 RT is essential for cell-type differentiation in Dictyostelium.";
 RL Genes Dev. 12:1525-1538 (1998).
 DR EMBL; AF019985; AAB70844.1; -
 DR HSSP; P35813; IAG0.
 DR InterPro; IPR001019; Gproteinh_alpha.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00503; G-alpha_1.
 DR Pfam; PF00481; PP2C_1.
 DR ProDom; PD000281; Gproteinh_alpha; 1.
 DR SMART; SM00275; G-alpha; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C; 1.
 DR PROSITE; PS01032; PP2C_1.
 SQ SEQUENCE 975 AA; 109916 MW; BBB322F5026D2A4F CRC64;

Query Match 18.2%; Score 368; DB 5; Length 975;
 Best Local Similarity 28.1%; Pred. No. 3.5e-21;
 Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;
 QY 8 PEPERSPPPAKGAQKQGLLPFDLPASSTSGSGGFLPFDLPASSGDSGLATIS 67
 DB 620 PKPPEKPKPT--KEPKKPVK-BSKPPEK-----PKPIKPKKSKPKPK 661
 QY 68 QNVKTEGKANKRTS-----EEKNGSEEL--VEKKVCKASSVIFGLKGVAKRGE 117
 DB 662 KEPKTKPKPKKRTSKYDGAESKKNKGADSCNGVSGIKLESG--FG-----SLQGR 713
 QY 118 REEMQDAHVILNDITEECR--PPSSLLITRVSYAVFDHGGRASKFAAONLHQLI-- 172
 DB 714 RKNMBDTHVILNNMGAVYVNGPCKDI--PISYAVYVHGCGTSTLLEPTPHNCLVNS 771
 QY 173 RKFPKGDVISEKTVKRCCLDTFKTDEEFLKQASSQKPAWKDSTATCVLAVDNLYIA 232
 DB 772 QSFPRGD-----YEQAFRDAVAEADIVIEKE-----KSGSTGVSAVLVGNKYTA 818
 QY 233 NGDSRAILCRYNESQKHAALS--LSKEHNPTQYEEBMRIOKAGGNVBDGRVLGL 287
 DB 819 NVGDSIEVLARQANAPKPGPVYEPVLLSYKHLASDDQEKRRVTDGLGMIIFNRLFGL 876

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OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:03 ; Search time 39 Seconds

(without alignments)
1339.340 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPEPRSPRPAK.....KAVRGSLDNTVTVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
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3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	22	AA828791 Human hydrolase-1i
2	2018	100.0	392	22	AB805726 Human signal trans
3	2018	100.0	421	22	AB812317 Human protein phos
4	2018	100.0	421	22	AA40555 Human polypeptide
5	2018	100.0	441	22	AAU23566 Novel human enzyme
6	2018	100.0	446	22	AAU22933 Novel human enzyme
7	2015	99.8	392	22	AA82585 Human protein sequ
8	2014	99.8	392	22	AA83769 Human polypeptide
9	1457.5	72.2	378	22	ABG09937 Novel human diagno
10	928	46.0	221	22	ABG09936 Novel human diagno

11	533.5	26.4	211	22	ABG07619 Novel human diagno
12	447.5	22.2	138	22	AAU23252 Novel human enzyme
13	431.5	21.4	295	21	AA818068 Arabidopsis thalia
14	431.5	21.4	305	21	AA818067 Arabidopsis thalia
15	404	20.0	86	21	AA803424 Human secreted pro
16	391.5	19.4	219	21	AA818065 Arabidopsis thalia
17	370.5	18.4	353	23	AB87579 Arabidopsis thalia
18	370.5	18.4	354	23	AA806997 Arabidopsis thalia
19	366.5	18.2	360	21	AA816902 Arabidopsis thalia
20	366.5	18.2	383	21	AA818038 Arabidopsis thalia
21	366.5	18.2	420	21	AA818038 Arabidopsis thalia
22	364	18.0	454	23	AB808338 Arabidopsis thalia
23	364	18.0	358	21	AA818041 Arabidopsis thalia
24	364	18.0	358	21	AA818041 Arabidopsis thalia
25	364	18.0	359	21	AA818040 Arabidopsis thalia
26	364	18.0	359	21	AA818040 Arabidopsis thalia
27	363	18.0	309	21	AA806998 Arabidopsis thalia
28	358.5	17.8	361	23	AA826620 Arabidopsis thalia
29	353.5	17.5	355	21	AA83887 Arabidopsis thalia
30	353.5	17.5	438	22	AA82980 Arabidopsis thalia
31	353.5	17.5	438	22	AA815376 Arabidopsis thalia
32	352.5	17.5	434	22	AA801344 Arabidopsis thalia
33	352	17.4	276	21	AA816903 Arabidopsis thalia
34	350	17.3	357	21	AA843237 Arabidopsis thalia
35	349	17.3	329	21	AA843238 Arabidopsis thalia
36	346	17.1	327	21	AA843888 Arabidopsis thalia
37	345.5	17.1	434	22	AA801348 Arabidopsis thalia
38	341.5	16.9	236	21	AA846904 Arabidopsis thalia
39	341	16.9	322	21	AA843239 Arabidopsis thalia
40	339	16.8	320	21	AA843895 Arabidopsis thalia
41	338.5	16.8	383	21	AA809824 Arabidopsis thalia
42	338	16.7	382	23	AB857063 Arabidopsis thalia
43	337.5	16.7	387	21	AA872963 Arabidopsis thalia
44	336	16.7	367	22	AB862019 Arabidopsis thalia
45	336	16.7	362	23	AB861491 Arabidopsis thalia

ALIGNMENTS

RESULT 1	AA828791	standard; Protein; 392 AA.
ID	AA828791	
AC	AA828791	
DT	13-FEB-2001	(first entry)
XX		
XX		Human hydrolase-like molecule 2 protein.
XX		
XX		Hydrolase-like molecule; human; cell proliferation disorder;
KW		autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
OS		Homo sapiens.
PN	US6132964-A.	
XX		
PD	17-OCT-2000.	
XX		
PF	06-FEB-1998;	98US-0013881.
XX		
PR	06-FEB-1998;	98US-0013881.
XX		
PA	(INCYTE) INCYTE PHARM INC.	
XX		
PI	Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;	
XX	WPI, 2001-006133/01.	
DR	N-PSDB; AAC60224.	
XX		
PT	New human hydrolase-like molecules (HHLMs) and polynucleotides encoding	
PT	the HHLMs, useful for diagnosing, treating or preventing cell	
PT	proliferation (e.g. bone cancer) or autoimmune disorders (e.g. AIDS or	

Query	MDLFGDLP	PEPERSPP	PAGKEAQ	KGPLF	FDLP	PPASSTDS	GGGGLF	FDLP	PPASSGDSG	60
1	MDLFGDLP	PEPERSPP	PAGKEAQ	KGPLF	FDLP	PPASSTDS	GGGGLF	FDLP	PPASSGDSG	60
1	MDLFGDLP	PEPERSPP	PAGKEAQ	KGPLF	FDLP	PPASSTDS	GGGGLF	FDLP	PPASSGDSG	60
61	SLATSI	SGMVT	TEGKG	AKRKT	SEEEK	NSSEEL	VEKVK	CKASSV	IGLKG	YAEKGEREE
61	SLATSI	SGMVT	TEGKG	AKRKT	SEEEK	NSSEEL	VEKVK	CKASSV	IGLKG	YAEKGEREE
61	SLATSI	SGMVT	TEGKG	AKRKT	SEEEK	NSSEEL	VEKVK	CKASSV	IGLKG	YAEKGEREE
121	MODAHV	ILNDITE	CECR	PPSSLI	TRVSY	PAVPD	HGIGI	PASKFA	PAONL	HONLIRKFKCDV
121	MODAHV	ILNDITE	CECR	PPSSLI	TRVSY	PAVPD	HGIGI	PASKFA	PAONL	HONLIRKFKCDV
121	MODAHV	ILNDITE	CECR	PPSSLI	TRVSY	PAVPD	HGIGI	PASKFA	PAONL	HONLIRKFKCDV
181	ISVEKTV	RCLDP	TFKHT	DEEFL	KASSOK	PAWKGS	ATATCV	LAANDN	LYIAN	IGDSRAI
181	ISVEKTV	RCLDP	TFKHT	DEEFL	KASSOK	PAWKGS	ATATCV	LAANDN	LYIAN	IGDSRAI
181	ISVEKTV	RCLDP	TFKHT	DEEFL	KASSOK	PAWKGS	ATATCV	LAANDN	LYIAN	IGDSRAI
241	LCRNYE	ESQKAA	LSLS	KEHNP	PTYEE	RMRI	OKAGAN	RDGVL	GLVE	VSRSIGGOYKR
241	LCRNYE	ESQKAA	LSLS	KEHNP	PTYEE	RMRI	OKAGAN	RDGVL	GLVE	VSRSIGGOYKR
241	LCRNYE	ESQKAA	LSLS	KEHNP	PTYEE	RMRI	OKAGAN	RDGVL	GLVE	VSRSIGGOYKR
301	CGVTSV	PDIR	RCQLT	PNDR	FILL	ACDGL	FKVFT	PEAVN	FILS	CLEDEKIQ
301	CGVTSV	PDIR	RCQLT	PNDR	FILL	ACDGL	FKVFT	PEAVN	FILS	CLEDEKIQ
301	CGVTSV	PDIR	RCQLT	PNDR	FILL	ACDGL	FKVFT	PEAVN	FILS	CLEDEKIQ
361	ARYEAC	NRLANK	AVOR	GSADN	VTM	VVRIGH	392			
361	ARYEAC	NRLANK	AVOR	GSADN	VTM	VVRIGH	392			
361	ARYEAC	NRLANK	AVOR	GSADN	VTM	VVRIGH	392			

XX	WP1; 2002-055860/07.
DR	N-PSDB; ABA93763.
XX	
PT	Human cDNA sequences and clones derived from human fetal brain, fetal
PT	kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
PT	screening and therapy -
XX	
PS	Claim 1; Page 377; 61pp; English.
XX	
CC	The present invention describes assemblies and computer readable media
CC	comprising novel human cDNA sequences and clones derived from human
CC	fetal brain, fetal kidney, melanoma, testis and amygdala cDNA
CC	libraries. ABA93762 to ABA93766 represent human cDNA sequences from the
CC	present invention which encode the proteins given in ABB05662 to
CC	ABB05729. The human cDNA sequences and clones can be used in gene
CC	therapy. The clones may be used in a variety of applications, for
CC	example they may be used in profiling assays, for providing large arrays
CC	of human genetic material for implementing large-scale screening
CC	strategies and for treating diseases via gene therapy procedures.
XX	
SQ	Sequence 392 AA;
Query Match	100.0%; Score 2018; DB 23; Length 392;
Best Local Similarity	100.0%; Pred. No. 5.7e-187;
Matches 392; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MDLFGDLPEDERSDPRAAGKEAKGKPLLFDDLPASSTDSGGPDLFDDLPPASSGDSC 60
OY	1 MDLFGDLPEDERSDPRAAGKEAKGKPLLFDDLPASSTDSGGPDLFDDLPPASSGDSC 60
Db	1 MDLFGDLPEDERSDPRAAGKEAKGKPLLFDDLPASSTDSGGPDLFDDLPPASSGDSC 60
OY	61 SLATSIQMYKTBEKGAKRKRTSEBKSGSELVEKKVCASVTFGLKGVAEKKGEREE 120-
Db	61 SLATSIQMYKTBEKGAKRKRTSEBKSGSELVEKKVCASVTFGLKGVAEKKGEREE 120
OY	121 MODAHVLNLTITEECRPPSLITRVSYFAVPFDGHGIRASKFAAQNHLIRKFPKGV 180
Db	121 MODAHVLNLTITEECRPPSLITRVSYFAVPFDGHGIRASKFAAQNHLIRKFPKGV 180
OY	181 ISVEKYTKRCCLDTFKHTDEEFLLQAASSOKPAWMDGSTATCVLANIDILYIANIGDSRAI 240
Db	181 ISVEKYTKRCCLDTFKHTDEEFLLQAASSOKPAWMDGSTATCVLANIDILYIANIGDSRAI 240
OY	241 LCRYNESQKHAAISLSKENHPTOYEBRMRIQKAGGNVRDGRVUGYLEVSRISDGQYKR 300
Db	241 LCRYNESQKHAAISLSKENHPTOYEBRMRIQKAGGNVRDGRVUGYLEVSRISDGQYKR 300
OY	.301 CGYVSVDIRCOLTPNDRFLIACDGLPKVFPEEAVNFLTSLCEDEKIOTREKGSAD 360
Db	.301 CGYVSVDIRCOLTPNDRFLIACDGLPKVFPEEAVNFLTSLCEDEKIOTREKGSAD 360
OY	361 ARYEACNRLANKAIVQSGSADNTVMVVVRIGH 392
Db	361 ARYEACNRLANKAIVQSGSADNTVMVVVRIGH 392
RESULT 3	
ABBI2317	
ID	ABBI2317 standard; peptide; 421 AA.
XX	
AC	ABBI2317;
XX	
DT	11-JAN-2002 (first entry)
XX	
DE	Human protein phosphatase 2C homologue, SEQ ID NO:2687.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW	haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW	inhibin; chemokinesis; chemokinesis; thrombolysis; oncogenesis;
KW	proliferation; metastasis; cancer; tumor; haematopoietic disorder;
KW	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW	chronic inflammatory condition; proliferative retinopathy;
KW	atherosclerosis; coronary heart disease; arterial ischaemia;

bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antihistaminic; antidiabetic; haemostatic; antileukosclerotic;
cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
antitumoral; antiviral; anticancer.
Homo sapiens.
MO200157188-A2.
09-AUG-2001.
05-FEB-2001; 2001WO-US03800.
03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Drmanac RT;
WPI: 2001-457740/49.
N-PSDB: ABA09561.
Human proteins and DNA encoding sequences useful for preventing,
treating or ameliorating a medical condition in a mammalian subject
e.g. arthritis and cancer -
Claim 20; Page 330; 1963pp; English.
Sequences ABB10981-ABB1330 represent 1350 novel human polypeptides, and
sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
invention also relates to vectors and recombinant host cells comprising a
nucleotide of the invention, methods of producing the novel polypeptides,
antibodies against the polypeptides, methods of detecting the nucleotides
or polypeptides in a sample, and methods of identifying compounds which
bind to polypeptides of the invention. Although novel, many of the
polypeptides of the invention have homology to known proteins, thereby
giving an insight into their probable biological activities, and hence
potential therapeutic applications. The polypeptides of the invention may
have various activities, including cytokine, cell proliferation or cell
differentiation activities; stem cell growth factor activity;
haematopoietic regulatory activity; tissue growth factor activity;
immunomodulatory activity; activin- or inhibin-related activities;
chemokine or chemokine-like activities; haemostatic, thrombotic or
thrombolytic activities; receptor or ligand activities; or may be
involved in oncogenesis; cancer cell proliferation or metastasis.
Depending on their biological activities, polypeptides and nucleotides of
the invention are useful for preventing, treating or ameliorating medical
conditions, e.g., by protein or gene therapy. Such conditions include
cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
proliferative retinopathy, atherosclerosis, coronary heart disease,
arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
vascular growth. Polypeptides involved with tissue regeneration and
repair (or nucleic acids encoding them) may be used to promote wound
healing (e.g., of burns, incisions and ulcers), while those with
immunomodulatory activities may be used in the treatment of viral,
bacterial and fungal infections in addition to immune disorders.
Polypeptides with growth factor activity may be used in cell cultures to
promote cell growth. For example, such polypeptides may be used to
manipulate stem cells in culture to give rise to neuroepithelial cells
that can be used to augment or replace cells damaged by illness,
autoimmune disease or accidental damage. The polypeptides and nucleotides
may also be used in the diagnosis of the above conditions, and in drug
screening techniques. The present sequence represents a novel human
polypeptide of the invention.

Query Match 100.0%; Score 2018; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 6,4e-187;
Sequence 421 AA;

Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPPEPRAPPAKEAOKPPLFDLPASSDSSGGLPFDLPASSGSG 60
Db 30 MDLFGDLPPEPRAPPAKEAOKPPLFDLPASSDSSGGLPFDLPASSGSG 89
QY 61 SLATSIQWVTEGKAKKRTSEBEKNGSEELVEKVCASVIFGLKGVAEKGEREE 120
Db 90 SLATSIQWVTEGKAKKRTSEBEKNGSEELVEKVCASVIFGLKGVAEKGEREE 149
QY 121 MODAHVILNDITECPSPSLITRVSYFAVDGCHGIRASKFAQNLHONLIRKPKGDV 180
Db 150 MODAHVILNDITECPSPSLITRVSYFAVDGCHGIRASKFAQNLHONLIRKPKGDV 209
QY 181 ISVEKTKRCGLDTPFGHTEEFKQASSQKAMKDSQATCVAVNIIYIANTLDSRAI 240
Db 210 ISVEKTKRCGLDTPFGHTEEFKQASSQKAMKDSQATCVAVNIIYIANTLDSRAI 269
QY 241 LCRYNESQKHAALSKKEHNPLOYEERMRIOKAGNVRRGVGLVFSRSIGGOYKR 300
Db 270 LCRYNESQKHAALSKKEHNPLOYEERMRIOKAGNVRRGVGLVFSRSIGGOYKR 329
QY 301 CGVTSVPDTRCQLTRENDFILLACDGLFKVFTPEEAVNFIISLCEDEKLOTREKSAAD 360
Db 330 CGVTSVPDTRCQLTRENDFILLACDGLFKVFTPEEAVNFIISLCEDEKLOTREKSAAD 389
QY 361 ARYEACNRLANKAVORGSAADVTVVVRIGH 392
Db 390 ARYEACNRLANKAVORGSAADVTVVVRIGH 421

RESULT 4
AAM40555
ID AAM40555 standard; Protein: 421 AA.
XX AAM40555;
AC AAM40555;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 5486.
XX
XX Human; noctropin; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemostatic;
chemokine; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
XX
OS Homo sapiens.
PN WO20015312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
PF 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou F, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB: AAI5711.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS

XX Example 2; SEQ ID NO 5486; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA38642-AA44213) with neurotropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 421 AA:

Query Match 100.0%; Score 2018; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 6.4e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPERSPPRAAGKEAKGKPLFDLPASTDSGSGGPLLFDLPASSGDSG 60
DB 30 MDLFGDLPERSPPRAAGKEAKGKPLFDLPASTDSGSGGPLLFDLPASSGDSG 89
QY 61 STATISQWKTGKAGKAKRTSEENKSGSELYEKVCKASSYIFGLKGVAKRGERE 120
DB 90 STATISQWKTGKAKKRTSEENKSGSELYEKVCKASSYIFGLKGVAKRGERE 149
QY 121 MODAHVILNDITEECRPPSLITRVSYFAVFDGSGIRASKFAAQMHLNLRKPKGDV 180
DB 150 MODAHVILNDITEECRPPSLITRVSYFAVFDGSGIRASKFAAQMHLNLRKPKGDV 209
QY 181 ISEKTVKRCCLDFTFHTDEEFLKQASSQKPAKDKSTATCVLAVNNIYIANLGSRAI 240
DB 210 ISEKTVKRCCLDFTFHTDEEFLKQASSQKPAKDKSTATCVLAVNNIYIANLGSRAI 269
QY 241 LCRVNEESGKAALSLSKENPFOYEEHRIQAGGNVBDGRLVGLVSRISGDSQYR 300
DB 270 LCRVNEESGKAALSLSKENPFOYEEHRIQAGGNVBDGRLVGLVSRISGDSQYR 329
QY 301 CGVTSPDIRRCQLTENDRFLILACDGLFKVFTPEEAVNFILSCLDEKIQTRREGKSAAD 360
DB 330 CGVTSPDIRRCQLTENDRFLILACDGLFKVFTPEEAVNFILSCLDEKIQTRREGKSAAD 389
QY 361 ARYEAAACNRLANKAVORGSAADNTVAVRIGH 392.
DB 390 ARYEAAACNRLANKAVORGSAADNTVAVRIGH 421

RESULT 5

AAU23566
ID AAU23566 standard; Protein; 441 AA.

AC AAU23566;

DT 17-DEC-2001 (first entry)

XX Novel human enzyme polypeptide #652.

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;

KM nephrotropic; anticoagulant.

OS Homo sapiens.

PN WO200155301-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01239.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0215647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226881.

PR 22-AUG-2000; 2000US-0226868.

PR 23-AUG-2000; 2000US-0227182.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0228287.

PR 01-SEP-2000; 2000US-0229342.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229512.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0233397.

PR 14-SEP-2000; 2000US-0233398.

PR 14-SEP-2000; 2000US-0233399.

PR 14-SEP-2000; 2000US-0233400.

PR 14-SEP-2000; 2000US-0233401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235814.
PR 27-SEP-2000; 2000US-0235814.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0235827.
PR 29-SEP-2000; 2000US-0235867.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0244826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249247.
PR 17-NOV-2000; 2000US-0249248.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250360.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465566/50.
DR N-PSDB; AAS41436.
XX
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
XX Claim 11; SEQ ID No 1562; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 441 AA;
SQ
Query Match 100.0%; Score 2018; DB 22; Length 441;
Best local Similarity 100.0%; Pred. No. 6, 9e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPPEPERSPPRAAGKEAKOKPLFDLPASSSTDSGSGPLFDLPASSGSDSG 60
DB 50 MDLFGDLPPEPERSPPRAAGKEAKOKPLFDLPASSSTDSGSGPLFDLPASSGSDSG 109
QY 61 SLATSIOMYKTEGKAKRKTSEEEKNGSEBELVEKKVCASSVITGLKGYAERKGEREE 120
DB 110 SLATSIOMYKTEGKAKRKTSEEEKNGSEBELVEKKVCASSVITGLKGYAERKGEREE 169
QY 121 MODAHVILNDITEECPPPSLITRYSYFAVFDGGGIRASKERAONLHONIRFPFGDV 180
DB 170 MODAHVILNDITEECPPPSLITRYSYFAVFDGGGIRASKERAONLHONIRFPFGDV 229
QY 181 ISVEKTVKRCGLDTPFGHDEEFLKQASSOKPAWKDOSTATCYLAVNDILYIANIGDSRAI 240
DB 230 ISVEKTVKRCGLDTPFGHDEEFLKQASSOKPAWKDOSTATCYLAVNDILYIANIGDSRAI 289
QY 241 LCRYNESQKHAALSIKKNHPTQYEEPMRIQKAGGVNDGKVLGVLEVSISIDGQYKR 300
DB 290 LCRYNESQKHAALSIKKNHPTQYEEPMRIQKAGGVNDGKVLGVLEVSISIDGQYKR 349
QY 301 CGVTSVPDIRRCQLTENDFILLACDGLFKVFTPEEAVNFILISCLEDEKIOTRGKSAAD 360
DB 350 CGVTSVPDIRRCQLTENDFILLACDGLFKVFTPEEAVNFILISCLEDEKIOTRGKSAAD 409
QY 361 ARYEACNRLANKAVORGSGADNVTVMYVRIGH 392
DB 410 ARYEACNRLANKAVORGSGADNVTVMYVRIGH 441
RESULT 6
AAU22933
ID AAU22933 standard; Protein; 446 AA.

XX AAU22933;
AC 17-DEC-2001 (first entry)
DT Novel human enzyme polypeptide #19.
DE
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW 11ase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX Homo sapiens.
OS
XX WO200155301-A2.
PN
PD 02-AUG-2001.
17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 28-JUN-2000; 2000US-0209467.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

	01-DEC-2000;	2000US-025031.	PR
	05-DEC-2000;	2000US-025103.	PR
	05-DEC-2000;	2000US-025198.	PR
	05-DEC-2000;	2000US-025671.	PR
	06-DEC-2000;	2000US-025147.	PR
	08-DEC-2000;	2000US-025185.	PR
	08-DEC-2000;	2000US-025186.	PR
	08-DEC-2000;	2000US-025189.	PR
	08-DEC-2000;	2000US-025199.	PR
	11-DEC-2000;	2000US-025407.	PR
	03-JAN-2001;	2001US-025678.	XX
FA	(HUMA-) HUMAN GENOME SCI INC.		FA
P1	Rosen CA, Barash SC, Ruben SM;		P1
XX	WPI; 2001-465566/50.		XX
DR	N-PSDB; AAS40803.		DR
XX			XX
PT	Novel polypeptides and polynucleotides useful for diagnosing,		PT
	preventing, treating neural, immune system, muscular, reproductive,		
	pulmonary, cardiovascular, renal, proliferative disorders and cancerous		
	diseases -		
XX			XX
SS	Claim 11; SEQ ID NO 929; 1180bp; English.		SS
CC	The present invention relates to the isolation of novel human enzyme		CC
CC	polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences		CC
CC	encoding them. The enzyme polypeptides of the invention may comprise the		CC
CC	functional classes of oxidoreductases, transferases, hydrolases, lyases,		CC
CC	isomerases or liasess. The sequences of the invention are useful in the		CC
CC	diagnosis, treatment, prevention and/or prognosis of a wide range of		CC
CC	disorders, including hyperproliferative disorders (e.g. cancer),		CC
CC	immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.		CC
CC	e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),		CC
CC	metabolic disorders (e.g. phenylketonuria), inflammatory disorders		CC
CC	(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),		CC
CC	blood-related disorders (e.g. haemophilia), reproductive disorders		CC
CC	(e.g. infertility) and infectious disorders (e.g. influenza). The		CC
CC	polynucleotides of the invention can also be used in gene therapy.		CC
CC	AU022915-AU023814 represent the novel human enzyme polypeptides of the		CC
CC	invention.		CC
CC	Note: The sequence data for this patent did not form part of the printed		CC
CC	specification, but was obtained in electronic format directly from WIPO		CC
CC	at ftp.wipo.int/pub/published_pct_sequences.		CC
XX			XX
SQ	Sequence 446 AA:		SQ
	100.0%; Score 2018; DB 22; Length 446;		
	Matches 392; Conservative 0; Mismatched 0; Indels 0; Gaps 0		
OY	1 MDLFGDLPEPERSRPPAAKGAKGFLFDPLPPASSDSSGGPLFDLPDPASSGSG 60		OY
Dd	55 MDLFDDLEPERSPRPAAKGEAKGFLFDPLPPASTDSSGGPLFDLPDPASSGSG 115		Dd
OY	61 SLATSIOMVWTBEGKARKTSEEEKNGSEELVEKKVKASVIFGLKGVAMERGFEE 120		OY
Dd	115 SLATSIOMVWTBEGKARKTSEEEKNGSEELVEKKVKASVIFGLKGVAMERGFEE 170		Dd
OY	121 MODAVIILNDITTECRPSSLIRVSYPVAFPGHGCIAPSKFAFPAONIHQLIRPKGDV 180		OY
Dd	175 MODAHVILNDITECRPSSLIRVSYPVAFPGHGCIAPSKFAFPAONIHQLIRPKGDV 230		Dd
OY	181 ISVERTVRCCLDTDFPKATDEEPLKOASSOKPAMKDGSATCVLAVDNLIYIANLGDSRAI 240		OY
Dd	235 ISERTVRCCLDTDFPKATDEEPLKOASSOKPAMKDGSATCVLAVDNLIYIANLGDSRAI 290		Dd
OY	241 LCRYNEESOKIAALSLSEKHNPFOYEERNRIQACGANVRGRVLGLEVASRTIGDOYKR 300		OY
Dd	295 LCRYNEESOKIAALSLSEKHNPFOYEERNRIQACGANVRGRVLGLEVASRTIGDOYKR 350		Dd

OY 301 CGGATSVDPPIRCQCTGNDDEFILACDGGFKVFPTPEEYVNFILSCDEDEIOTRGSKSAD 362
 Db 355 CGGATSVDPPIRCQCTGNDDEFILACDGGFKVFPTPEEYVNFILSCDEDEIOTRGSKSAD 414
 OY 361 ARYEACNRLANKAYORGADVTVMYRIH 392
 Db 415 ARYEACNRLANKAYORGADVTVMYRIH 446
 RESULT 7
 AAB92585
 ID AAB92585 standard; Protein; 392 AA.
 AC AAB92585;
 DE 26-JUN-2001 (first entry)
 DT
 XX Human protein sequence SEQ ID NO:10816.
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 F1 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 P1 WPI; 2001-318749/34.
 XX
 XX
 PS Claim 8; SEQ ID 10816; 2537bp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC polynucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH11628 and
 CC AAH11633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 392 AA;
 XX

Query Match 99.9%; Score 2015; DB 22; Length 392;
 Best Local Similarity 99.7%; Pred. No. 1.4e-186;
 Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPPASTDSGSGGPLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPPASTDSGSGGPLLFDLPPASSGDSG 60
 QY 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 DB 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 QY 121 MODAHVILNDITEECPSPSLITRVSYPFVFDHGIGIRASKFAAQNHLONLIRKPKGDV 180
 DB 121 MODAHVILNDITEECPSPSLITRVSYPFVFDHGIGIRASKFAAQNHLONLIRKPKGDV 180
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLADNLIYIANLGDSPRAI 240
 DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLADNLIYIANLGDSPRAI 240
 QY 241 LCRVNEESQKHAALSLSKEHNPTQYEEHRIQKAGNVDRGVGLVLEVSRSIGDQGYR 300
 DB 241 LCRVNEESQKHAALSLSKEHNPTQYEEHRIQKAGNVDRGVGLVLEVSRSIGDQGYR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSGADNVTVMVVRIGH 392

RESULT 8

ID AAM38769 standard; Protein; 392 AA.

XX AAM38769;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 1914.

XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;

KW chemokine; chromolytic; drug screening; arthritis; inflammation;

KW Leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.
 DR N-PSDB; AA157925.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -

Example 3; SEQ ID NO 1914; 10078pp; English.

CC The invention relates to human nucleic acids (AA157928-AA161369) and
 CC the encoded polypeptides (AAM38642-AA442213) with nocotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification.

Sequence 392 AA:

Query Match 99.8%; Score 2014; DB 22; Length 392;
 Best Local Similarity 99.7%; Pred. No. 1.4e-186;
 Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPPASTDSGSGGPLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPPASTDSGSGGPLLFDLPPASSGDSG 60
 QY 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 DB 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 QY 121 MODAHVILNDITEECPSPSLITRVSYPFVFDHGIGIRASKFAAQNHLONLIRKPKGDV 180
 DB 121 MODAHVILNDITEECPSPSLITRVSYPFVFDHGIGIRASKFAAQNHLONLIRKPKGDV 180
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLADNLIYIANLGDSPRAI 240
 DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLADNLIYIANLGDSPRAI 240
 QY 241 LCRVNEESQKHAALSLSKEHNPTQYEEHRIQKAGNVDRGVGLVLEVSRSIGDQGYR 300
 DB 241 LCRVNEESQKHAALSLSKEHNPTQYEEHRIQKAGNVDRGVGLVLEVSRSIGDQGYR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSGADNVTVMVVRIGH 392

RESULT 9

ID ABG09937 standard; Protein; 378 AA.

XX ABG09937;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #9928.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW Food supplement; medical imaging; diagnostic; genetic disorder.


```

XX OS Homo sapiens.
XX OS
XX PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX N-PSDB; AAS74124.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID No 40296; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful for medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 AA;
XX
XX Query Match 72.2%; Score 1457.5; DB 22; Length 378;
XX Best Local Similarity 77.9%; Pred. No. 1.3e-132;
XX Matches 303; Conservative 13; Mismatches 46; Indels 27; Gaps 6;
XX
XX QY 20 KEAOKPPLFDLPPASSTDSGSGPPLFDLPPASSGDSGLATISIQWTEGKQAKR 79
XX Db 1 KEAOKPPLFDLPPASSTPSA-----VAALGTTPSPVTLWFLQTRRSKIWRN 49
XX
XX QY 80 KTSBEKNGSEELVKKYCK-----ASVTFPLKQYVVERGSEEMODAHVI 127
XX Db 50 SLDYQSKVAEPWCHERQOKADRFGLGRGVNPASSVTFPLKQYVVERGSEEMODAHVI 109
XX
XX QY 128 LNDITECRPPSLITRYSYPAVDGCGGRAPKFAQONLIRKPKPDVSVYKTV 187
XX Db 110 LNDITECRPPSLITRYSYPAVDGCGGRAPKFAQONLIRKPKPDVSVYKTV 169
XX
XX QY 188 KRCLDLPFHTEDEEFLKQASSOKPAMKDGSTATCVAVNIIYINLSDSAILCRNNE 247
XX Db 170 KRCLDLPFHTEDEEFLKQASSOKPAMKDGSTATCVAVNIIYINLSDSAILCRNNE 229
XX
XX QY 248 SOKHAALSLSKENHTQYEEBMRIOKAGNVGRGLVGLVYSRISGGQYKRCGV-TSV 306
XX Db 230 SOKHAALSLSKENHTQYEEBMRIOKAGNVGRGLVGLVYSRISGGQYKRCGCHLCA 289

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QY 307 PDIRCOLTPNDRFILL-ACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEA 365
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Db 230 PFSRCQLTNPDRFILWPCDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYLRS 349
XX |||||
QY 366 A-CNRLANKAVRGCS-ADNVTVMVVRIGH 392
XX |||||
Db 350 SPATRLANKAVAAAGARPQVTVTVVVRIGH 378
XX |||||
XX
XX RESULT 10
XX ABG09936
XX ID ABG09936 standard; Protein; 221 AA.
XX
XX AC ABG09936;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #9927.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX N-PSDB; AAS74123.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID No 40295; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful for medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SO Sequence 221 AA;
XX
XX Query Match 46.0%; Score 928; DB 22; Length 221;

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Best Local Similarity 95.4%; Pred. No. 1.5e-81;
Matches 184; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 MDLFGDPEPERSPRPAKGEAKGGLLPDDLPPASSTDS-----GSGGLLPDDL 52
DB 30 MDLFGDPEPERSPRPAKGEAKGGLLPDDLPPASSTDSGLQALPGSGGLLPDDL 89

QY 53 PASSGDSGLATSIQWVTEKGAKRKTSSEENKNGSELVEKVCASVIFGLKGYA 112
DB 90 PASSGDSGLATSIQWVTEKGAKRKTSSEENKNGSELVEKVCASVIFGLKGYA 149

QY 113 ERKGEREMQDAVILNDITEECRPPSLITRVSYFVFPDGHGIRASKRAQNLHONLI 172
DB 150 ERKGEREMQDAVILNDITEECRPPSLITRVSYFVFPDGHGIRASKRAQNLHONLI 209

QY 173 RKFPKGDVISE 184
DB 210 RKFPKGDVISE 221

LT 11
ABG07619
ID ABG07619 standard; Protein; 211 AA.
AC ABG07619;
XX 13-FEB-2002 (first entry)
DT Novel human diagnostic protein #7610.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.
XX MO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS71806.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID No 37978; 103bp; English.

The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 211 AA:

Query Match 26.4%; Score 533.5; DB 22; Length 211;
Best Local Similarity 61.4%; Pred. No. 2.6e-43;
Matches 124; Conservative 11; Mismatches 54; Indels 13; Gaps 5;

QY 204 KOASSQKPMW----KDSITATCVLAVDNTLYIANLGDSDA---ILCRYNESQKHALSI 256
DB 10 RONGSSKPLMLXGSGAOKSVYEVKPLLPQMIQHARRPCLQACSSRPAPASI 69

QY 257 SKHNPTQYEEBRIQ---KAGNVDRGVLGVEVSRISIDGOYKRCGVTSVPDIRRC 312
DB 70 PSSSPTARDTKHRAQVKTTDSGARRRDGRVGLVSVSISADGOYKRCGVTSVPDIRRC 129

QY 313 QLTPLN-DRFILLACDGLFVFTPEEAVNFIISCLBDEKIQTREKSAADARIEAQNRLA 371
DB 130 QLTPOXPGSILLACDGLFVFTPEEAVNFIISCLBDEKIQTREKSAADARIEAQNRLA 189

QY 372 NKAVORGK-ADNVTVMVVRIGH 392
DB 190 NKAVVAAGARPDNVTVMVVRIGH 211

RESULT 12
AAU23252
ID AAU23252 standard; Protein; 138 AA.
AC AAU23252;
XX 18-DEC-2001 (first entry)
XX
XX Novel human enzyme polypeptide #338.
DE
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
XX Homo sapiens.
XX
XX WO200155301-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01239.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 18-APR-2000; 2000US-0190076.
XX 19-MAY-2000; 2000US-0198123.
XX 07-JUN-2000; 2000US-0205515.
XX 28-JUN-2000; 2000US-0209467.
XX 30-JUN-2000; 2000US-0214886.
XX 07-JUL-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.

CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 138 AA;

Query Match 22.2%; Score 447.5; DB 22; Length 138;
Best Local Similarity 87.4%; Pred. No. 3.1e-35;
Matches 90; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

Qy 279 RDGRVLGVLEVERSRISDGGYKRCGVTSPDIRCOLTPNDRIILLACDGLFKVFTPEEAV 338
Db 10 RGRVGLGVLEVERSRISDGGYKRCGVTSPDIRCOLTPNDRIILLACDGLFKVFTPEEAV 69

Qy 339 NFILSCLEDEKIQTRREGKSAADARYEAACNRLANK-AVORGSA 380
70 NFILSCLEDEKIQTRREGKSAADARYEAALQHGQCGCGRGSX 112

RESULT 13

AAIG18068
ID AAG18068 standard; Protein; 295 AA.

XX AAG18068;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 19329.

KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.

XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.

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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160988.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 21.4%; Score 431.5; DB 21; Length 305;

Best Local Similarity 37.2%; Pred. No. 3,6e-33;

Matches 102; Conservative 59; Mismatches 86; Indels 27; Gaps 8;

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QY 78 KRRTSEERKNGSEELV-----EKKVCASSVI-----FGLKGYAVERKGEREEMODAHVI 127
    |||||
    34 KAKSEEVSGCGEAVAAVGNREAEEDKPSFVSEKKEFLVEADVADKGAHMTMEDVWTV 93
    |||||
QY 128 LNDITEECRPSSLIITRVSYFAVFDGCGIRASKFAAQNLTQNLIRKPKGDVYSVEKTV 187
    |||||
DB 94 LPDASLDF--PGLT--RCAHFAIYDGHGRLAEFAKKHMLNLVLSAGLPRELLDV-KVA 148
    |||||
QY 188 KRCLDTPFKHTDEEFLKQASSOKPAMKDSSTATCVAVNLTLYANIGDSRAIICR----- 243
    |||||
DB 149 KKALEGFRKIDELLQKSVS--CGMQDGAIVACWIIDQKVFVANITQDAKAVIARSSTT 206
    |||||
QY 244 -----YNESQKHALSLSKENHTQVEEMRIQKAGNV-RDGVYGVLEVRSIGDQ 297
    |||||
DB 207 NELGNHTGANPLKAIYIRHKAIYQENSRLOKSGGVYISSNGRLQRLVSAFQDNH 266
    |||||
QY 298 YKRCGVTSVPDIRRCQLTPNDRFILLACDGLFVY 331
    |||||
DB 267 FKRFVSAITPDIAFELTERENFWILCDGLMEV 300
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RESULT 15

AAG03424

ID AAG03424 standard; Protein; 86 AA.

AC AAG03424;

DT 06-OCT-2000 (First entry)

XX Human secreted protein, SEQ ID NO: 7505.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping.

XX Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

XX (GENSET) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR N-PSDB; AAC03430.

XX WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 13; SEQ ID 7505; 71pp + CD-ROM; English.

PS The present sequence is a polypeptide encoded by one of a large number
 of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 were prepared from total human RNAs or polyA+ RNAs derived from 30
 different tissues. EST sequences usually correspond mainly to the 3'
 untranslated region (UTR) of the mRNA because they are often obtained
 from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 those cases where longer cDNA sequences have been obtained, the full 5'
 UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 ends and can therefore be used to obtain full length cDNAs and genomic
 DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 chromosome mapping procedures. They are used to obtain upstream
 regulatory sequences and to design expression and secretion vectors.

XX Sequence 86 AA;

Query Match 20.0%; Score 404; DB 21; Length 86;

Best Local Similarity 92.9%; Pred. No. 2.5e-31;

Matches 79; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 121 MODAHVILNDITEECRPSSLIITRVSYFAVFDGCGIRASKFAAQNLTQNLIRKPKGDV 180
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DB 1 MODAHVILNDITEECRPSSLIITRVSYFAVFDGCGIRASKFAAQNLTQNLIRKPKGDV 60
    |||||
QY 181 ISVEKTVKRCILDTPFKHTDEEFLKQ 205
    |||||
DB 61 ISVEKTVKRCILDTPFKHTDEEFLKQ 85
    |||||

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Search completed: June 7, 2003, 09:36:55

Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:06 ; Search time 15 Seconds
(without alignments)
768,919 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPBPRSPRPAK.....KAVRGADNVTVVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: /cgn2_6/ptodaca/1/1aa/SR_COMB.pep:*
2: /cgn2_6/ptodaca/1/1aa/SB_COMB.pep:*
3: /cgn2_6/ptodaca/1/1aa/EA_COMB.pep:*
4: /cgn2_6/ptodaca/1/1aa/6S_COMB.pep:*
5: /cgn2_6/ptodaca/1/1aa/PCOTS_COMB.pep:*
6: /cgn2_6/ptodaca/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	4	US-09-013-881-2
2	1618	16.8	306	2	US-08-822-701-8
3	340	16.8	306	3	US-08-935-855-8
4	320.5	15.9	309	4	US-09-206-646-4
5	320.5	15.9	309	3	US-08-822-701-7
6	319	15.8	390	2	US-08-935-855-7
7	319	15.8	390	4	US-08-822-701-3
8	317.5	15.7	281	2	US-08-822-701-9
9	317.5	15.7	281	3	US-08-935-855-9
10	313	15.5	478	2	US-08-873-093-1
11	313	15.5	478	4	US-09-206-646-1
12	271.5	13.5	314	2	US-08-822-701-10
13	271.5	13.5	314	3	US-08-935-855-10
14	269.5	13.4	392	2	US-08-822-701-2
15	269.5	13.4	392	3	US-08-935-855-12
16	269.5	13.4	542	3	US-08-935-855-20
17	255.5	12.7	546	3	US-08-935-855-22
18	178	8.8	504	2	US-08-752-891-2
19	178	8.8	504	4	US-09-144-178-2
20	178	8.8	504	4	US-09-406-854-2
21	178	8.8	504	4	US-09-529-279-2
22	178	8.8	504	4	US-09-529-279-3
23	178	8.8	513	4	US-09-529-279-11
24	176	8.7	504	2	US-08-752-891-6
25	176	8.7	504	2	US-09-144-178-6
26	176	8.7	504	2	US-09-144-178-6
27	176	8.7	504	2	US-09-144-178-6

28	176	8.7	504	4	US-09-406-854-6	Sequence 6, Appl1
29	125	6.2	249	4	US-09-134-001C-4777	Sequence 4777, Ap
30	107	5.3	273	1	US-08-320-161-10	Sequence 10, Appl
31	107	5.3	273	4	US-08-455-829-10	Sequence 10, Appl
32	107	5.3	273	4	US-08-235-836C-13	Sequence 13, Appl
33	107	5.3	273	4	US-08-455-973-10	Sequence 10, Appl
34	103	5.1	475	4	US-09-370-838-193	Sequence 193, App
35	100.5	5.0	466	4	US-08-235-836C-107	Sequence 107, App
36	96.5	4.8	1085	1	US-08-431-080-28	Sequence 28, Appl
37	96.5	4.8	1085	2	US-08-938-534-28	Sequence 28, Appl
38	96.5	4.8	1085	4	US-09-345-294-28	Sequence 28, Appl
39	95	4.7	447	4	US-09-916-109-5	Sequence 5, Appl1
40	95	4.7	483	4	US-09-916-109-5	Sequence 4, Appl1
41	94.5	4.7	422	2	US-09-067-351-3	Sequence 3, Appl1
42	94.5	4.7	422	4	US-09-360-490-3	Sequence 3, Appl1
43	92.5	4.6	2756	1	US-08-375-709-11	Sequence 11, Appl
44	92.5	4.6	2756	1	US-08-752-929-11	Sequence 11, Appl
45	92.5	4.6	2756	4	US-09-090-793-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-013-881-2
Sequence 2, Application US/0903881
Patent No. 6132964
GENERAL INFORMATION:
APPLICANT: Bardman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Cortey, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purni
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILKINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT02
CLONE: 195647
US-09-013-881-2

Query Match 100.0%; Score 2018; DB 4; Length 392;
 Best Local Similarity 100.0%; Pred. No. 6.8e-201;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPPEPRPPRAAGKEAKGKGLPDDLPASTDSGSGPILFPDLPASSGDSG 60
 DB 1 MDLFGDLPPEPRPPRAAGKEAKGKGLPDDLPASTDSGSGPILFPDLPASSGDSG 60
 QY 61 STATISOWKVTGKAKRKTSEEEKNGSEBELVEKVCASSVIFGLKGVARKGEREE 120
 DB 61 STATISOWKVTGKAKRKTSEEEKNGSEBELVEKVCASSVIFGLKGVARKGEREE 120
 QY 121 MODAHVILNDITEBCRPSSILTRVSYFAVFDGHGIRASKFAQNLHQLIRKPKGDV 180
 DB 121 MODAHVILNDITEBCRPSSILTRVSYFAVFDGHGIRASKFAQNLHQLIRKPKGDV 180
 QY 181 ISEKTVKRCCLDITFGHTDEEFLKQASSQKPAKDGSTATCVLAUNILYIANLGSRAI 240
 DB 181 ISEKTVKRCCLDITFGHTDEEFLKQASSQKPAKDGSTATCVLAUNILYIANLGSRAI 240
 QY 241 LCRVNESQKHAALSLSKENHPTQYEBRMIOKAGNVDRVLGVLEVSRSIGDQYKR 300
 DB 241 LCRVNESQKHAALSLSKENHPTQYEBRMIOKAGNVDRVLGVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCQLTENDREFILLACDGLPKVFTPEBAVNFILSCLEDEKIQTRGKSAD 360
 DB 301 CGVTSVPDIRRCQLTENDREFILLACDGLPKVFTPEBAVNFILSCLEDEKIQTRGKSAD 360
 QY 361 ARYEACNRLANKAVORGSGADNTVWVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSGADNTVWVVRIGH 392

RESULT 2

US-08-822-701-8
 Sequence 8, Application US/08822701
 Patent No. 5976853

GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Rattus
 US-08-822-701-8

Query Match 16.8%; Score 340; DB 2; Length 306;
 Best Local Similarity 33.7%; Pred. No. 6e-27;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLKGYAERKGEREEMODAHVILNDITEBCRPSSILTRVSYFAVFDGHGIRASKFAQ 165
 DB 21 GLRYGLSSMQGWRVEMEDAHVIGL-----PSGLLET-WSPFAVYDGHAGSQVAKYCE 73
 QY 166 NIHLNLIKRP-KED--VISVEKTVKRCCLDITFGHTDEEFLKQASSQKPAKDGSTATCV 222
 DB 74 HLDDHITNNQDRKSGAGAPSVK-NVKNIGIRTFLEIDEMRVMSKKGAGADSGSTAVGV 132
 QY 223 LAVNDILYIANLGDRAILCRVNESQKHAALSLSKENHPTQYEBRMIOKAGNVDRGR 282
 DB 133 LISPHITFINGDSDRLCR-----NRKVHFTQDKPSPNPLEKERIQNAGSVMIOR 186
 QY 283 VLGVLVSRISIGDQYKRC---GVT-----SVPDIRRCQLTENDREFILLACDGLFK 330
 DB 187 VNGSLAVSRALDPDFYK-CVHGKGPTEQLVSPPEVHDIERSE--EDQFILLACDGIWD 243
 QY 331 VFTPEBAVNFILSCLE--DEKIQTRGKSADARYEACNRLANKAVORGSGADNTVWV 388
 DB 244 VNGNEELCDFVNSRLEVTID-----LEKVCNEVVDTCLYKSGHDNMSVILI 289

RESULT 3

US-08-935-855-8
 Sequence 8, Application US/08935855
 Patent No. 6066485

GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/935,855
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Rattus
 US-08-935-855-8

Query Match 16.8%; Score 340; DB 3; Length 306;
 Best Local Similarity 33.7%; Pred. No. 6e-27;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLKGYAERKGEREMODAHVILNDITECRPPSSILITVSYFAVFDHGIGIRASKFAAQ 165
 DB 21 GLRYGLSSMOGWREMEDAHTAVIGL-----PSGLET-WSPFAVYDGHASQVAKYCE 73
 QY 166 NLHONLRKRP-KGD--VISYKTVKRCLLDTEKHTDEEFLKQASSOKPAWKDSTATCV 222
 DB 74 HLDHITNNQDFKSGAGAPSYE--VKNKGIPTGLEIDEIMRWSEKKGADRSOSTAVGV 132
 QY 223 LAVDNILYIANIGDSRAILCRYNESOKHAALSLSEKHNPTOYEEHMRIOKAGNVADGR 282
 DB 133 LISPHQHTYFINGDSRGLLCR-----NRKVHFPTQDHKPSNPLEKERIQWAGGSVMIOG 186
 QY 283 VLGVLEVSRSIGDQGYKRC---GVT-----SYPDIRRCQLTPNDRFILACDGLPK 330
 DB 187 VNGSLAVSRALGDPYK-CVNGKGPTEQLVSPPEVHDIERE--EDDQFILACGSDMD 243
 QY 331 VFTPEAVNFILSCLE--DEKIQTRBKSAADARVAAACNPLANKAVORGADNVYTMV 388
 DB 244 VMGNELCDPFRSRLVETD-----LEKVCNEVVDICLYKSRDMVSIVILI 289

RESULT 4
 US-09-206-646-4
 Sequence 4, Application US/09206646
 Patent No. 643637
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Goli, Suriya K.
 APPLICANT: Lal, Preeti G.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
 FILE REFERENCE: PF-0319-1 DIV
 CURRENT APPLICATION NUMBER: US/09/206,646
 CURRENT FILING DATE: 2001-12-07
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PERL Program
 SEQ ID NO 4
 LENGTH: 390
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: ID No. 6436637 g452526
 US-09-206-646-4

Query Match 16.2%; Score 326; DB 4; Length 390;
 Best Local Similarity 30.0%; Pred. No. 2.5e-25;
 Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;

QY 78 KRKTSEEEKNGSEELVEKKVKASVIFGLKGYAERKGEREMODAHVILNDITECRP 137
 DB 7 KPKTEKNAHAGN-----GLRYGLSSMOGWREMEDAHTAVVGI----- 46
 QY 138 PSSLITRVSYFAVFDHGIGIRASKFAAONLHONL-----IRKPK-GDVI--SVYKTVR 189
 DB 47 PHGL-DNWSFFAVYDGHASRVANVCSHLEHITTEDFRAADSGSALSPSYE-SVKT 104
 QY 190 CLDTEKHTDEEFLKQASSOKPAWKDSTATCVLAVDNILYIANIGDSRAILCRYNESQ 249
 DB 105 GIRTGLFKTIDEYMRNFSDLRNGMDRSGSTAVGVWVPTHTMYFINGDSRAVLCNNG--- 161

QY 250 KHAALSLSEKHNPTOYEEHMRIOKAGNVDRGVILGVLEVSRSIGDQGYKRCG----- 302
 DB 162 ---VCFSTQHKRCNCEVEKERIQNAGSSVMIOQUNGSILASRALGDPYDKCDGSGPTQ 218
 QY 303 -VTSVPDIRRCQLTPNDRFILACDGLPKVTPPEANFILTSGDEBKIQTRBKSAADA 361
 DB 219 LVSPPEYEVETVAEDEFVILACDGIWDVMSNEELCEPYSKRL-----VSD 266
 QY 362 RYEAACRLANKAVORGADNVYTMV 388
 DB 267 DLENVCNVVDTCLHKSRDMNSVVLV 293

RESULT 5
 US-08-822-701-7
 Sequence 7, Application US/08822701
 Patent No. 597683
 GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 APPLICANT: Basilio, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS: 18
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 US-08-822-701-7

Query Match 15.9%; Score 320.5; DB 2; Length 309;
 Best Local Similarity 29.7%; Pred. No. 6.5e-25;
 Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

QY 78 KRKTSEEEKNGSEELVEKKVKASVIFGLKGYAERKGEREMODAHVILNDITECRP 137
 DB 7 KPKTEKNAHAGN-----GLRYGLSSMOGWREMEDAHTAVVGI----- 46
 QY 138 PSSLITRVSYFAVFDHGIGIRASKFAAONLHONL-----IRKPK-GDVI--KTV 187
 DB 47 PHGL-DNWSFFAVYDGHASRVANVCSHLEHITTEDFRAADSGSALSPSYEVSXVG 105
 QY 188 KRCLDTEKHTDEEFLKQASSOKPAW-KDGSATATCVLAVDNILYIANIGDSRAILCRYN 246

Db 106 RTGFLKI-----DEYKMFSDLRNGMDRSGSTAAGVWVSPTTHMYFINCGSRALVLCRNQ 160
QY 247 ESQKHAALSKEHNPTQYEERMRIOKAGNVRDGVGLVEVSRISIGDQYKRCG-----302
Db 161 -----VCSFTQDHKPCNPVEKERIQVAGSVMIQKRVNSLAVSRALGDYKCVDGKGP 214
QY 303 ----VTSVPDIRCOLTPNDRFILACDGLFKVFTPEEAVNFILSCLEDEKIQTEBKSA 358
Db 215 TEQVSPPEPEVEIYVRAEDEFFVLACDGIWDMVMSNEELCEFKSRLE-----262
QY 359 ADARYEACNRLANKAVQSGADNVTVMVY 388
Db 263 VSDDLNVCNMVYDTCLHKGRDMSVLY 292

RESULT 6
US-08-935-855-7
Sequence 7, Application US/08935855

GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-935-855-7

Query Match 15.9%; Score 320.5; DB 3; Length 309;
Best Local Similarity 29.7%; Pred. No. 6,5e-25;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

QY 78 KRKTSSEKNGSEELVEKVKVCASSVIFGLKGYAERKGEREEMODAVIINDITECRP 137
Db 7 KRKTEKHNHAGN-----GLRYGLSSMGQWRVEMEDAHAVVGI-----46
QY 138 PSSLLTRVYFAVFDGHRGIRASKFAAQLHONL-----IRKPK-GDVI--SVE--KTV 187

Db 47 PHGL-DNMSFAVYDGHAGSVANYCSTHLEHTTNEDFRAADKSGSALBSPVESVKTG 105
QY 188 KCLDLTFKHTDEEFLKQASSOKPAM-KDGSTATCVLANDNLTLYIANLGDSSRAILCRVNE 246
Db 106 RTGFLKI-----DEYKMFSDLRNGMDRSGSTAAGVWVSPTTHMYFINCGSRALVLCRNQ 160
QY 247 ESQKHAALSKEHNPTQYEERMRIOKAGNVRDGVGLVEVSRISIGDQYKRCG-----302
Db 161 -----VCSFTQDHKPCNPVEKERIQVAGSVMIQKRVNSLAVSRALGDYKCVDGKGP 214
QY 303 ----VTSVPDIRCOLTPNDRFILACDGLFKVFTPEEAVNFILSCLEDEKIQTEBKSA 358
Db 215 TEQVSPPEPEVEIYVRAEDEFFVLACDGIWDMVMSNEELCEFKSRLE-----262
QY 359 ADARYEACNRLANKAVQSGADNVTVMVY 388
Db 263 VSDDLNVCNMVYDTCLHKGRDMSVLY 292

RESULT 7
US-08-873-093-3
Sequence 3, Application US/08873093

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1247927

US-08-873-093-3

Query Match 15.8%; Score 319; DB 2; Length 390;
Best Local Similarity 29.4%; Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

QY 78 KRKTSSEKNGSEELVEKVKVCASSVIFGLKGYAERKGEREEMODAVIINDITECRP 137

Db 7 KPKTEKHNAGN-----GLRYGLSSMGWRVEMEDAHAVVGI-----46
QY 138 PSSLIIRVSYFVAFDGHGIRASFAAONLHOL-----IRKFPKGVY---SVEKTVK 189
Db 47 PGL-EDMSFFAVYGHAGSVANVYCSHLEHITTNEDFRAADSGFALPSE-NVKT 104
QY 190 CLIDTFKHTDEEFLKQASSOKPAWKDSTATCVLAVDNILYANIGDSRAILCRVNEBQ 249
Db 105 GRTGFLKIDETMRNFSDLRNGMRSGSTAVGMSPTHITFINGDSRAVLCNQ---161
QY 250 KAAALSLSKENHPTQYERMRITQAGGNVDGVLGVLEVSRSIGDQYRCG-----302
Db 162 ---VCFSTODHKPCNPKERIQNAGGSVMICQVNSLAVSALDDYKCVDGKPTQ 218
QY 303 -VTSVPDIRCOLTJPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSADA 361
Db 219 LVSPEVEYELRAEDEFVVLACDGIWDMVMSNEELCEFNVRLE-----VSD 266
QY 362 RYEAACNRLANKAVRGSDNVTVMV 388
267 DLENVCNWWVDTCILHKSGRDMISIVL 293

RESULT 8
US-09-206-646-3
Sequence 3, Application US/09206646
Patent No. 643637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319-1 DIV
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: ID No. 643637 9247927
US-09-206-646-3

Query Match 15.8%; Score 319; DB 4; Length 390;
Best Local Similarity 29.4%; Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;
Db 78 KRTTSEKNGSEELVEKKVCKASSVIFGLKGVVAERKGERENODAHVILNDITECRP 137
Db 7 KPKTEKHNAGN-----GLRYGLSSMGWRVEMEDAHAVVGI-----46
QY 138 PSSLIIRVSYFVAFDGHGIRASFAAONLHOL-----IRKFPKGVY---SVEKTVK 189
Db 47 PGL-EDMSFFAVYGHAGSVANVYCSHLEHITTNEDFRAADSGFALPSE-NVKT 104
QY 190 CLIDTFKHTDEEFLKQASSOKPAWKDSTATCVLAVDNILYANIGDSRAILCRVNEBQ 249
Db 105 GRTGFLKIDETMRNFSDLRNGMRSGSTAVGMSPTHITFINGDSRAVLCNQ---161
QY 250 KAAALSLSKENHPTQYERMRITQAGGNVDGVLGVLEVSRSIGDQYRCG-----302
Db 162 ---VCFSTODHKPCNPKERIQNAGGSVMICQVNSLAVSALDDYKCVDGKPTQ 218
QY 303 -VTSVPDIRCOLTJPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSADA 361
Db 219 LVSPEVEYELRAEDEFVVLACDGIWDMVMSNEELCEFNVRLE-----VSD 266
QY 362 RYEAACNRLANKAVRGSDNVTVMV 388

Db 267 DLENVCNWWVDTCILHKSGRDMISIVL 293

RESULT 9
US-08-822-701-9
Sequence 9, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guttridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-822-701-9

Query Match 15.7%; Score 317.5; DB 2; Length 281;
Best Local Similarity 31.4%; Pred. No. 1.1e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;
QY 111 VAERKGE--REEMODAHVILNDITECRPSSLIIRV--SYPAVFDGHGIRASFAAON 166
Db 23 VAENKNSKFRITMEDHTVKNFA-----SRIDMGYFVAFGHAGIOASKWCKH 72
QY 167 LH-----ONLIRKFPKGVISVEKTVKCLIDTFKHTDEEFLKQASSOKPAWKDST-ATC 221
Db 73 LHITIEONIL-----ADETRDVRLVNSFLAIDEEI-----NTKLVGNSGCTAAVC 119
QY 222 VL---AVDNI-----LYIANIGDSRAILCRVNEBQKAAALSLSKENHPTQY 265
Db 120 VLRLNELPDSVSDSMDLAHQKRLTYANVGDSTRIVLFRNN-----SIRLYDHKASDT 173
QY 266 EEMRIQKAGGNVDGVLGVLEVSRSIGDQYRCGVTSPDIRCOLTJPNDRFILLAC 325
Db 174 LEMRVBQAGGLIMKSRVNGMLAVTRSLGDKFFDSLVGS-PFTTSVEITSEDKFLILAC 232
QY 326 DGLFKVFTPEEAVNFILSCLEDEKIQTRGKSADARRYEAACNRLANKAVRGSDNVTVM 385

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Db      233 DGLMDVIDDQDACELIKQITEPNE-----AAKVLVRALENGTIDNTV 276
Oy      386 MVV 388
Db      277 MVV 279

RESULT 10
US-08-935-855-9
: Sequence 9, Application US/08935855
: Patent No. 6066485
: GENERAL INFORMATION:
: APPLICANT: Guthridge, Mark
: APPLICANT: Basiglio, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/935,855
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 281 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM: Saccharomyces cerevisiae
: US-08-935-855-9

Query Match      15.7%: Score 317.5; DB 3; Length 281;
Beet Local Similarity 31.4%: Pred. No. 1.1e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12.

Oy      111 VAEKRGK--REEMODAHVILNDITEBCKPPSSLIIRV--SYFAVPDGGGIRASKFAAON 166
Db      23 VAENKNSKFRKTMEVHTYVKNFA-----SRIDMGFIAYVDGAGIQAASKMGKH 72
Oy      167 LH----QNLIRKFPKGDVIVSEKTVKRCLLDTFKATDEFLKQASQKPAWKDGT-ATC 221
Db      73 LHTIIEQNIL-----ADETRDVDRVLDNSFLAIDBEI-----NPTLVNGSGCTAAVC 119
Oy      222 VL---AVDNT-----LYIANLGDGRALICYNBESQGAALSLSKENPTQY 265
Db      120 VLRMELPDSVSDSDMDLAQHQRKLYTANVGDSTRIVLFNGN-----SIRLTYDHKASDT 173
Oy      266 EERRIRIQAGGNVDRGVLGVLEVSRSISGDQYKRCGTVSPDIRRCQLTNDPFIILAC 325
Db      174 LEMQRFVEAGGLIMKSRVNGMLAVTRSLGDKFDFSLVVG--PFTTSVETSEDKFLIILAC 232

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QY      326  DGLKRVFPEEAVNFILSLCEDEKIQTEEGKSADARYEACNRLANAVORGSDANTV 385
Db      233  DGLMDVDIDDOACELIKDITPEN-----AAKVLVRVALENGTIDNTV 276

QY      386  MVV 388
Db      277  MVV 279

RESULT 11
US-08-873-093-1
; Sequence 1, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goll, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPLIB01
; CLONE: 13177
; US-08-873-093-1

Query Match      15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 7.8e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps

QY      78  KRKTSSEERKSGSELVEKKVCASSVIFGLGVYAERGEREEMODAHVILINDITEECRP 137
Db      7  KPRTKEKNMAGAGN-----GLRYGLSSMGQWVEVEDATATVAGI----- 46

QY      138  PSSLIITVSYFAVDGCGIRASKFPAQNTLHQNLIR-----KPKGDIYSVEKTVKR 189
Db      47  PHGI-EDMSPFAVVDGAGSRVANYCSTHLLEHTTNEDFPAAGSGSGALELVE- NVKN 104

QY      190  CLDITFGHTDEEFLKQASSQKPAKKDGSATCAVLAVNIIYIALNGDSRALTCRNESQ 249
Db      105  GIRTGFLKIDYEMNFSDLRNGMDRSGSTAVGVMISPHGVIIFINCGDSRAVLVYRNGQ--- 161

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QY 250 KHAALSLSKENHPYOEEBMRIOKAGGNVADGVLGVLEVSRIIDGGOYKRCG-----302
Db 162 ---VCFSTQDHKPCNPREKERIONAGGSVMIOQVNGSLAVSRALGDYKCVDGKGPTEQ 218
QY 303 -VTSVPDIRRCQULTPNDRFILLACDGLFKYFTPEEAVNFIISCLEDEKIQTRREGSKAADA 361
Db 219 LVSPPEVEYILRAEDEFIILLACDGLWDVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVORGADNVTVMV 388
Db 267 DLENVCNWWVDTCILHKSRDNNISVLV 293

RESULT 12
US-08-873-093-4
Sequence 4, Application US/08873093
Patent No. 585397
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873_093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1452526
US-08-873-093-4

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 7.8e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY 78 KRKTSEBKNGSEELVEKKVKASSVIFGLKGYVAERKGEREMODAHVILNDITEECRP 137
Db 7 KPRTKKNMAGAGN-----GLRYGLSSMGWRVEMEDAHAVVGI-----46
QY 138 PSSLITRVSYFAVPFDGHGIRASKPAQNLHONLIR-----KPKGDVTSVEKTYKR 189
Db 47 PHGL-EDWSFFAVYDGHGASRVANYCSTHLEHTTNEDEPRAAGKSGSALEISVE-NVKN 104

QY 190 CLDTPKHTDEEFLKOASSOKPAMKDGSTATCVLAVDNIIYANLGDSPAILCRYNESQ 249
Db 105 GIRGFLKIDEVWRNFSDLRNGMDSRSGSTAVGVMSIPKHIFYINCDSRAVLVRNGQ---161
QY 250 KHAALSLSKENHPYOEEBMRIOKAGGNVADGVLGVLEVSRIIDGGOYKRCG-----302
Db 162 ---VCFSTQDHKPCNPREKERIONAGGSVMIOQVNGSLAVSRALGDYKCVDGKGPTEQ 218
QY 303 -VTSVPDIRRCQULTPNDRFILLACDGLFKYFTPEEAVNFIISCLEDEKIQTRREGSKAADA 361
Db 219 LVSPPEVEYILRAEDEFIILLACDGLWDVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVORGADNVTVMV 388
Db 267 DLENVCNWWVDTCILHKSRDNNISVLV 293

RESULT 13
US-09-206-646-1
Sequence 1, Application US/09206646
Patent No. 643637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PR-0319-1 DIV
CURRENT APPLICATION NUMBER: US/09/206_646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6436637 013177CD1
US-09-206-646-1

Query Match 15.5%; Score 313; DB 4; Length 479;
Best Local Similarity 28.7%; Pred. No. 7.9e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY 78 KRKTSEBKNGSEELVEKKVKASSVIFGLKGYVAERKGEREMODAHVILNDITEECRP 137
Db 7 KPRTKKNMAGAGN-----GLRYGLSSMGWRVEMEDAHAVVGI-----46
QY 138 PSSLITRVSYFAVPFDGHGIRASKPAQNLHONLIR-----KPKGDVTSVEKTYKR 189
Db 47 PHGL-EDWSFFAVYDGHGASRVANYCSTHLEHTTNEDEPRAAGKSGSALEISVE-NVKN 104
QY 190 CLDTPKHTDEEFLKOASSOKPAMKDGSTATCVLAVDNIIYANLGDSPAILCRYNESQ 249
Db 105 GIRGFLKIDEVWRNFSDLRNGMDSRSGSTAVGVMSIPKHIFYINCDSRAVLVRNGQ---161
QY 250 KHAALSLSKENHPYOEEBMRIOKAGGNVADGVLGVLEVSRIIDGGOYKRCG-----302
Db 162 ---VCFSTQDHKPCNPREKERIONAGGSVMIOQVNGSLAVSRALGDYKCVDGKGPTEQ 218
QY 303 -VTSVPDIRRCQULTPNDRFILLACDGLFKYFTPEEAVNFIISCLEDEKIQTRREGSKAADA 361
Db 219 LVSPPEVEYILRAEDEFIILLACDGLWDVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVORGADNVTVMV 388
Db 267 DLENVCNWWVDTCILHKSRDNNISVLV 293

RESULT 14

US-08-822-701-10
Sequence 10, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Leishmania
US-08-822-701-10

Query Match 13.5%; Score 271.5; DB 2; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12;
Matches 84; Conservative 43; Mismatches 90;

116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASKFAAONLHONLIRKF 175
116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASKFAAONLHONLIRKF 175
31 GYREIMEDHNL-----TYLTDMSWGFVFDGIVNDQCGOYLERARRS----- 72
176 PKGDVIVSEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-----GSTATCVLAVDN--- 227
73 -----ALEK-----ESIPMTDERMKEALRIDQEMWDSGREGSGTGFVALKEGNK 119
228 -ILYIANLGDRAILCRVNEESQKHAALSLSKEHNPTQYEEEMRIQKAGGNVRDGRVGLV 286
120 VHLQVGNVDSRVAC-----IDGVCVPLTEDHKPNNEGERORLNCAGRVENNRVDS 173
287 LEVSRISIGGOYK-----RCGVTSVPDIRCQLT--PNDRFILLACDGLFK-VFTPEE 336
174 LAVSRAFGREYKLGSGSQLEQKVIYALADVQHKDFTPSND-FVLLCCDGVEGNFPNBE 232
337 AVNFIILSLEDKIQTRREGKSADARYEACN-----RLANKAVQSGADNVTVVVR 389
233 VVAIVKQOLE-----TCNDLAEVAGRVCEALERGSRDNISCMIVQ 273

RESULT 15
US-08-935-855-10

Sequence 10, Application US/08935855
Patent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Leishmania
US-08-935-855-10

Query Match 13.5%; Score 271.5; DB 3; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12;
Matches 84; Conservative 43; Mismatches 90;

116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASKFAAONLHONLIRKF 175
116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASKFAAONLHONLIRKF 175
31 GYREIMEDHNL-----TYLTDMSWGFVFDGIVNDQCGOYLERARRS----- 72
176 PKGDVIVSEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-----GSTATCVLAVDN--- 227
73 -----ALEK-----ESIPMTDERMKEALRIDQEMWDSGREGSGTGFVALKEGNK 119
228 -ILYIANLGDRAILCRVNEESQKHAALSLSKEHNPTQYEEEMRIQKAGGNVRDGRVGLV 286
120 VHLQVGNVDSRVAC-----IDGVCVPLTEDHKPNNEGERORLNCAGRVENNRVDS 173
287 LEVSRISIGGOYK-----RCGVTSVPDIRCQLT--PNDRFILLACDGLFK-VFTPEE 336
174 LAVSRAFGREYKLGSGSQLEQKVIYALADVQHKDFTPSND-FVLLCCDGVEGNFPNBE 232
337 AVNFIILSLEDKIQTRREGKSADARYEACN-----RLANKAVQSGADNVTVVVR 389
233 VVAIVKQOLE-----TCNDLAEVAGRVCEALERGSRDNISCMIVQ 273

Search completed: June 7, 2003, 09:37:41
Job time: 17 secs